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<140> PCT/GB2003/005664

<141> 2003-12-23

<150> GB 0230006.9

<151> 2002-12-23

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Tyr Asp

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<213> Homo sapiens

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Ser Ile Ile Pro Met Tyr Gly
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 ag 182

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 <213> Homo sapiens

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Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu
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Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg Asp
 35 40 45

Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly
 50 55 60

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 <211> 27
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 1 5 10 15

Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg

20

25

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 ctgcagccca agtggcccca ggccccgtgg gagag 155

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 Arg Gly Arg Gly
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 caaggcctgg agcaggtgcc ccgggtgttg ctcaggagca gtcctggctg gccggagtgt 300
 ccaccaagcc cacagtccca tcttcagaag caggaatcca gccagtcct gtccagggaa 360
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<210> 12
 <211> 139
 <212> PRT
 <213> Homo sapiens

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Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly
 35 40 45

Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala
 50 55 60

Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser
 65 70 75 80

Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu
 85 90 95

Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile
 100 105 110

Gln Pro Val Pro Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val
 115 120 125

Pro Arg Asn His Phe Lys Gly Met Ser Glu Asp
 130 135

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 <212> DNA
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 gccccagtg tccacatcgg ccagcgatgg aacctgagtg cctcggacat caccggggtc 540
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 cacagcactg gtaggagccc cgccccggcc tccctatctc tgcagcggct tttggaggca 660
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 <212> PRT
 <213> Homo sapiens

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 Glu Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp
 35 40 45
 Phe Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg
 50 55 60
 Ser Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys
 65 70 75 80
 Gly Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp
 85 90 95
 His Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp
 100 105 110
 Asn Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser
 115 120 125
 Ser Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly
 130 135 140
 Arg Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp
 145 150 155 160
 Ala Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp
 165 170 175
 Ile Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg
 180 185 190
 Pro Arg Gly Arg Gly Ser His Ala His Ser Thr Gly Arg Ser Pro Ala
 195 200 205
 Pro Ala Ser Leu Ser Leu Gln Arg Leu Leu Glu Ala Leu Ser Ala Glu
 210 215 220
 Ser Arg Ser Pro Asp Pro Ser Gly Ser Ser Ala Gly Gly Gln Pro Val
 225 230 235 240
 Pro Ala Gly Pro Gly Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu
 245 250 255
 Lys Lys Leu Ser Ala Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala
 260 265 270
 Ser Ser Pro Arg Ser Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln
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 Glu Gln Ser Trp Leu Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser
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<210> 20
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<212> PRT
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Ile Ile Arg Pro
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<210> 21
<211> 94
<212> DNA
<213> Homo sapiens

<400> 21
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gtggagggtcc ccttcctgct ctccagcaag tacg 94

<210> 22
<211> 32
<212> PRT
<213> Homo sapiens

<400> 22
Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met Gly
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Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp
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<210> 23
<211> 118
<212> DNA
<213> Homo sapiens

<400> 23
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tcaggtttgt cacctatcag gaccagagag acttcatttc catcatcccc atgtatgg 118

<210> 24
<211> 39
<212> PRT
<213> Homo sapiens

<400> 24
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Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile
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Ser Ile Ile Pro Met Tyr Gly
      35

<210> 25
<211> 182
<212> DNA
<213> Homo sapiens

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cgagcacacg cgggccgacc gggaccgcta tatccgtgtc aactggaacg agatcctgcc 180
ag 182

<210> 26
<211> 61
<212> PRT
<213> Homo sapiens

<400> 26
Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser Leu
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Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu Leu
      20              25              30

Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg Asp
      35              40              45

Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly
      50              55              60

<210> 27
<211> 82
<212> DNA
<213> Homo sapiens

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cctctgtgat gcactatggg ag 82

<210> 28
<211> 27
<212> PRT
<213> Homo sapiens

<400> 28
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1              5              10              15

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Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
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<210> 29
 <211> 155
 <212> DNA
 <213> Homo sapiens

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 ctgcagccca agtggcccca ggccccgtgg gagag 155

<210> 30
 <211> 52
 <212> PRT
 <213> Homo sapiens

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 1 5 10 15

Pro Ser Val His Ile Gly Gln Arg Trp Asn Leu Ser Ala Ser Asp Ile
 20 25 30

Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro
 35 40 45

Arg Gly Arg Gly
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<210> 31
 <211> 419
 <212> DNA
 <213> Homo sapiens

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 ccaccaagcc cacagtccca tcttcagaag cagggaatcca gccagtcctt gtccagggaa 360
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<210> 32
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 <213> Homo sapiens

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Leu Gln Arg Leu Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp

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35	40	45
Glu Ser Pro His Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala		
50	55	60
Glu Ala Ser Ala Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser		
65	70	75
Arg Pro Gly Ala Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu		
	85	90
Ala Gly Val Ser Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile		
	100	105
Gln Pro Val Pro Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val		
	115	120
Pro Arg Asn His Phe Lys Gly Met Ser Glu Asp		
130	135	

<210> 33
 <211> 1293
 <212> DNA
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ctggaggctc ttgcggagtt tgaacgttcc acgtgcatca ggtttgtcac ctatcaggac	420
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<210> 34
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 <212> PRT

<213> Homo sapiens

<400> 34

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20          25          30

Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln
35          40          45

Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu
50          55          60

Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg
65          70          75          80

Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met
85          90          95

Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr
100         105         110

Asp Glu Pro Ser Arg Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu
115         120         125

Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe
130         135         140

Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser
145         150         155         160

Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly
165         170         175

Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His
180         185         190

Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn
195         200         205

Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Arg Ser Ser
210         215         220

Asn Met Leu Thr Pro Tyr Asp Tyr Ser Ser Val Met His Tyr Gly Arg
225         230         235         240

Leu Ala Phe Ser Arg Arg Gly Leu Pro Thr Ile Thr Pro Leu Trp Ala
245         250         255

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Thr Arg Val Leu Lys Leu Tyr Gly Cys Ser Pro Ser Gly Pro Arg Pro

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gtccccttcc	tgctctccag	caagtacgat	gagcccagcc	gccagggtcat	cctggagggt	300
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gaccccagtg	gttccagtgc	gggagggccag	cccgttcctg	cagggcctgg	ggagagccca	960
catgggtggg	agtcctctgc	cctgaaaaag	ctcagtgcag	aggcctcggc	aaggcagcct	1020
cagaccctag	cttctctccc	aagatcaagg	cctggagcag	gtgcccccg	tgttgctcag	1080
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1224

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 Pro Ala Ile Asn Gln Gly Leu Ile Leu Glu Glu Thr Pro Glu Ser Ser
 35 40 45
 Phe Leu Ile Glu Gly Asp Ile Ile Arg Pro Ser Pro Phe Arg Leu Leu
 50 55 60
 Ser Ala Thr Ser Asn Lys Trp Pro Met Gly Gly Ser Gly Val Val Glu
 65 70 75 80
 Val Pro Phe Leu Leu Ser Ser Lys Tyr Asp Glu Pro Ser Arg Gln Val
 85 90 95
 Ile Leu Glu Ala Leu Ala Glu Phe Glu Arg Ser Thr Cys Ile Arg Phe
 100 105 110
 Val Thr Tyr Gln Asp Gln Arg Asp Phe Ile Ser Ile Ile Pro Met Tyr
 115 120 125
 Gly Cys Phe Ser Ser Val Gly Arg Ser Gly Gly Met Gln Val Val Ser
 130 135 140
 Leu Ala Pro Thr Cys Leu Gln Lys Gly Arg Gly Ile Val Leu His Glu
 145 150 155 160
 Leu Met His Val Leu Gly Phe Trp His Glu His Thr Arg Ala Asp Arg
 165 170 175
 Asp Arg Tyr Ile Arg Val Asn Trp Asn Glu Ile Leu Pro Gly Phe Glu
 180 185 190
 Ile Asn Phe Ile Lys Ser Arg Ser Ser Asn Met Leu Thr Pro Tyr Asp
 195 200 205
 Tyr Ser Ser Val Met His Tyr Gly Arg Leu Ala Phe Ser Arg Arg Gly
 210 215 220
 Leu Pro Thr Ile Thr Pro Leu Trp Ala Pro Ser Val His Ile Gly Gln
 225 230 235 240
 Arg Trp Asn Leu Ser Ala Ser Asp Ile Thr Arg Val Leu Lys Leu Tyr
 245 250 255

Gly Cys Ser Pro Ser Gly Pro Arg Pro Arg Gly Arg Gly Ser His Ala
 260 265 270
 His Ser Thr Gly Arg Ser Pro Ala Pro Ala Ser Leu Ser Leu Gln Arg
 275 280 285
 Leu Leu Glu Ala Leu Ser Ala Glu Ser Arg Ser Pro Asp Pro Ser Gly
 290 295 300
 Ser Ser Ala Gly Gly Gln Pro Val Pro Ala Gly Pro Gly Glu Ser Pro
 305 310 315 320
 His Gly Trp Glu Ser Pro Ala Leu Lys Lys Leu Ser Ala Glu Ala Ser
 325 330 335
 Ala Arg Gln Pro Gln Thr Leu Ala Ser Ser Pro Arg Ser Arg Pro Gly
 340 345 350
 Ala Gly Ala Pro Gly Val Ala Gln Glu Gln Ser Trp Leu Ala Gly Val
 355 360 365
 Ser Thr Lys Pro Thr Val Pro Ser Ser Glu Ala Gly Ile Gln Pro Val
 370 375 380
 Pro Val Gln Gly Ser Pro Ala Leu Pro Gly Gly Cys Val Pro Arg Asn
 385 390 395 400
 His Phe Lys Gly Met Ser Glu Asp
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<210> 37
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<400> 37
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 Ala Cys Gly Thr Ser Phe Pro Asp Gly Leu Thr Pro Glu Gly Thr Gln
 35 40 45
 Ala Ser Gly Asp Lys Asp Ile Pro Ala Ile Asn Gln Gly Leu Ile Leu
 50 55 60
 Glu Glu Thr Pro Glu Ser Ser Phe Leu Ile Glu Gly Asp Ile Ile Arg
 65 70 75 80
 Pro Ser Pro Phe Arg Leu Leu Ser Ala Thr Ser Asn Lys Trp Pro Met
 85 90 95

Gly Gly Ser Gly Val Val Glu Val Pro Phe Leu Leu Ser Ser Lys Tyr
 100 105 110
 Asp Glu Pro Ser His Gln Val Ile Leu Glu Ala Leu Ala Glu Phe Glu
 115 120 125
 Arg Ser Thr Cys Ile Arg Phe Val Thr Tyr Gln Asp Gln Arg Asp Phe
 130 135 140
 Ile Ser Ile Ile Pro Met Tyr Gly Cys Phe Ser Ser Val Gly Arg Ser
 145 150 155 160
 Gly Gly Met Gln Val Val Ser Leu Ala Pro Thr Cys Leu Gln Lys Gly
 165 170 175
 Arg Gly Ile Val Leu His Glu Leu Met His Val Leu Gly Phe Trp His
 180 185 190
 Glu His Thr Arg Ala Asp Arg Asp Arg Tyr Ile Arg Val Asn Trp Asn
 195 200 205
 Glu Ile Leu Pro Gly Phe Glu Ile Asn Phe Ile Lys Ser Gln Ser Ser
 210 215 220
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